## SEQUENCE LISTING <110> KAKKIS, EMIL D <120> METHODS FOR TREATING DISEASES CAUSED BY DEFICIENCIES OF RECOMBINANT ALPHA-L-IDURONDINASE <130> 008000051CNUS01 <140> TO BE ASSIGNED <141> 2001-11-13 <150> 09/711,205 <151> 2000-11-09 <150> 09/439,923 <151> 1999-11-12 <160> 2 <170> FastSEQ for Windows Version 3.0 <210> 1 <211> 6200 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (1558)...(3510) <400> 1 gacggatcgg gagatctccc gatcccctat ggtdgactct cagtacaatc tgctctgatg 60 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg 120 cgagcaaaat ttaagctaca acaaggcaag gctt\gaccga caattgcatg aagaatctgc 180 ttagggttag gegttttgeg etgettegeg atgtdeggge cagatataeg egttgacatt 240 gattattgac tagttattaa tagtaatcaa ttacggggtc attagttcat agcccatata 300 360 tggagttccg cgttacataa cttacggtaa atggc¢cgcc tggctgaccg cccaacgacc cccgcccatt gacgtcaata atgacgtatg ttcccdtagt aacgccaata gggactttcc 420 attgacgtca atgggtggac tatttacggt aaactgccca cttggcagta catcaagtgt 480 540 atcatatgcc aagtacgccc cctattgacg tcaatgacgg taaatggccc gcctggcatt 600 atgeceagta catgacetta tgggaettte etaettggea gtacatetae gtattagtea tegetattae catggtgatg eggttttgge agtacat|caa tgggegtgga tageggtttg 660 acteaegggg atttecaagt etecaeecea ttgaegtbaa tgggagtttg ttttggeace 720 aaaatcaacq qqactttcca aaatqtcqta acaactcdqc cccattqacq caaatqqqcq 780 gtaggcgtgt acggtgggag gtctatataa gcagagctct ctggctaact agagaaccca 840 ctgcttaact ggcttatcga aattaatacg actcactata gggagaccca agcttcgcag 900 aatteetgeg getgetaeag tgtgteeage gteetgeedg getgtgetga gegetggaae 960 agtggcgcat cattcaagtg cacagttacc catcctgagt ctggcacctt aactggcaca 1020 attgccaaag tcacaggtga gctcagatgc ataccagga& attgtatgac gttccctgct 1080 cacatgootg ctttcttcct ataatacaga tgctcaacta actgctcatg tccttatatc 1140 acagagggaa attggagcta tctgaggaac tgcccagaag\ggaagggcag aggggtcttg 1200 ctctccttgt ctgagccata actcttcttt ctaccttcca \text{gtgaacacct tcccacccca} 1260 ggtccacctg ctaccgccgc cgtcggagga gctggccctg attgagctct tgtccctgac 1320 atgcctggtg cgagctttca accctaaaga agtgctggtg dgatggctgc atggaaatga 1380 ggagctgtcc ccagaaagct acctagtgtt tgagccccta aaggagccag gcgagggagc 1440 caccacctac ctggtgacaa gcgtgttgcg tgtatcagct gaagcttga tatcgaattc 1500 cggaggcgga accggcagtg cagcccgaag ccccgcagtc cdcgagcacg cgtggcc atg 1560

Met

									ctg Leu 10									1608
									gcc Ala									1656
									ccc Pro									1704
									cac His									1752
									ctc Leu									1800
									acc Thr 90									1848
									ggc Gly									1896
	ctg Leu	gac Asp 115	gly aaa	tac Tyr	ctg Leu	gac Asp	ctt Leu 120	ctc\ Leu	agg Arg	gag Glu	aac Asn	cag Gln 125	ctc Leu	glà aaa	ttt Phe	gag Glu		1944
									ttc Phe									1992
>									gtc Val								:	2040
									gtt Val 170								:	2088
									ttt Phe								:	2136
								-	gcc Ala	_				_	_	_	:	2184
									ggc Gly								:	2232
									ggc Gly								:	2280

ggt Gly	acc Thr	aac Asn	ttc Phe 245	ttc Phe	act Thr	gly aaa	gag Glu	gcg Ala 250	Gly	gtg Val	cgg Arg	ctg Leu	gac Asp 255	tac Tyr	atc Ile	23	328
tcc Ser	ctc Leu	cac His 260	agʻg Argʻ	aag Lys	ggt Gly	gcg Ala	cgc Arg 265	agc Ser	tcc Ser	atc Ile	tcc Ser	atc Ile 270	ctg Leu	gag Glu	cag Gln	23	376
												ccc Pro				24	124
gac Asp 290	acc Thr	ccc Pro	att Ile	tac Tyr	aac Asn 295	gac Asp	gag Glu	gcg Ala	gac Asp	ccg Pro 300	ctg Leu	gtg Val	ggc Gly	tgg Trp	tcc Ser 305	24	172
ctg Leu	cca Pro	cag Gln	ccg Pro	tgg Trp 310	agg Arg	gcg Ala	gac Asp	gtg Val	acc Thr 315	tac Tyr	gcg Ala	gcc Ala	atg Met	gtg Val 320	gtg Val	25	520
												aac Asn				25	68
												ttc Phe 350				26	516
												cgc Arg				26	64
												aag Lys				27	12
												cag Gln				27	60
												cac His				28	08
gtc Val	ctg Leu	gcc Ala 420	agc Ser	gcc Ala	cac His	cgc Arg	ccc Pro 425	cag Gln	Gl <sup>A</sup> aac	ccg Pro	gcc Ala	gac Asp 430	gcc Ala	tgg Trp	cgc Arg	28	56
gcc Ala	gcg Ala 435	gtg Val	ctg Leu	atc Ile	tac Tyr	gcg Ala 440	agc Ser	gac Asp	gac Asp	acc Thr	cgc Arg 445	gcc Ala	cac His	ccc Pro	aac Asn	29	04
cgc Arg 450	agc Ser	gtc Val	gcg Ala	gtg Val	acc Thr 455	ctg Leu	cgg Arg	ctg Leu	cgc\ Arg	460 Gly 999	gtg Val	ccc Pro	ccc Pro	ggc Gly	ccg Pro 465	29	52
ggc Gly	ctg Leu	gtc Val	tac Tyr	gtc Val 470	acg Thr	cgc Arg	tac Tyr	ctg Leu	gac Asp 475	aac Asin	ggg Gly	ctc Leu	tgc Cys	agc Ser 480	ccc Pro	30	00
gac	ggc	gag	tgg	cgg	cgc	ctg	ggc	cgg	ccc	gtc	ttc	ccc	acg	gca	gag	30	48

Paly Cont

Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu 485 490 495	
cag ttc cgg cgc tag cgc gcg gct gag gac ccg gtg gcc gcg gcg ccc Gln Phe Arg Arg  * Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro 500	3096
cgc ccc tta ccc gcc ggc ggc cgc ctg agg ctg cgc ccc gcg ctg cgg Arg Pro Leu Pro Ala Gly Gly Arg Leu Arg Leu Arg Pro Ala Leu Arg 515 520 525	3144
ctg ccg tcg ctt ttg ctg gtg cac gtg tgt gcg cgc ccc gag aag ccg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala Arg Pro Glu Lys Pro 530 540	3192
ccc ggg cag gtc acg cgg\ctc cgc gcc ctg ccc ctg acc caa ggg cag Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln 545 550 560	3240
ctg gtt ctg gtc tgg tcg gat gaa cac gtg ggc tcc aag tgc ctg tgg Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp 565 570 575	3288
aca tac gag atc cag ttc tct cag gac ggt aag gcg tac acc ccg gtc Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val 580 585 590	3336
agc agg aag cca tcg acc ttc aac ctc ttt gtg ttc agc cca gac aca Ser Arg Lys Pro Ser Thr Phe Ash Leu Phe Val Phe Ser Pro Asp Thr 595 600 605	3384
ggt gct gtc tct ggc tcc tac cga gtt cga gcc ctg gac tac tgg gcc Gly Ala Val Ser Gly Ser Tyr Arg val Arg Ala Leu Asp Tyr Trp Ala 610 615 620	3432
cga cca ggc ccc ttc tcg gac cct gtg ccg tac ctg gag gtc cct gtg Arg Pro Gly Pro Phe Ser Asp Pro Val Pro Tyr Leu Glu Val Pro Val 625 630 635 640	3480
cca aga ggg ccc cca tcc ccg ggc aat cca tgagcctgtg ctgagcccca Pro Arg Gly Pro Pro Ser Pro Gly Asn Rro 645 650	3530
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<210> 2 <211> 650 <212> PRT

<213> Homo sapiens

<400> 2

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210 215 220 Thr Pro Pro Arg\Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His 230 235 Asp Gly Thr Asn the Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr 245 Ile Ser Leu His Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu 265 Gln Glu Lys Val Val Ala Gln Gln Ile Arg Gln Leu Phe Pro Lys Phe 280 Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala Asp Pro Leu Val Gly Trp 295 300 Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala Ala Met Val 310 Val Lys Val Ile Ala Gln\His Gln Asn Leu Leu Ala Asn Thr Thr 325 330 Ser Ala Phe Pro Tyr Ala Leu Ser Asn Asp Asn Ala Phe Leu Ser 345 Tyr His Pro His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln 360 Val Asn Asn Thr Arg Pro Pro His Val Gln Leu Leu Arg Lys Pro Val 375 Leu Thr Ala Met Gly Leu Leu \Ala Leu Leu Asp Glu Glu Gln Leu Trp 390 395 Ala Glu Val Ser Gln Ala Gly Thr Val Leu Asp Ser Asn His Thr Val 405 410 Gly Val Leu Ala Ser Ala His Atg Pro Gln Gly Pro Ala Asp Ala Trp 420 425 Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro 44 Q Asn Arg Ser Val Ala Val Thr Leu\Arg Leu Arg Gly Val Pro Pro Gly 455 460 Pro Gly Leu Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser 470 475 Pro Asp Gly Glu Trp Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala 485 490 Glu Gln Phe Arg Arg Arg Ala Ala Glu Asp Pro Val Ala Ala Ala Pro 50b Arg Pro Leu Pro Ala Gly Gly Arg Leu Arg Leu Arg Pro Ala Leu Arg 520 Leu Pro Ser Leu Leu Leu Val His Val\Cys Ala Arg Pro Glu Lys Pro 535 Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln Gly Gln 550 Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp 565 Thr Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val 585 Ser Arg Lys Pro Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr 600 Gly Ala Val Ser Gly Ser Tyr Arg Val Arg\Ala Leu Asp Tyr Trp Ala 615 620 Arg Pro Gly Pro Phe Ser Asp Pro Val Pro tyr Leu Glu Val Pro Val 630 Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro 645

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